



SEQUENCE LISTING

<110> Kilian, Andrzej
Bowtell, David

<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
THEREOF

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<140> 09/502,424

<141> 2000-02-11

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<170> PatentIn Ver. 2.0

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 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
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 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Thr Asp Thr Pro
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 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
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Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly
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ZINC
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INS
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 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 865 870 875 880

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
885 890 895

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
900 905 910

Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
915 920 925

Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
930 935 940

Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
945 950 955 960

Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
965 970 975

Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
980 985 990

Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
995 1000 1005

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
1010 1015 1020

Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
1025 1030 1035 1040

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
1045 1050 1055

His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
1060 1065 1070

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
1075 1080 1085

Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1090 1095 1100

<210> 5
<211> 884
<212> PRT
<213> Homo sapiens

<400> 5
Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
1 5 10 15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn

20 25 30
 Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
 35 40 45
 Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
 50 55 60
 Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
 65 70 75 80
 Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
 85 90 95
 Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
 100 105 110
 Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
 115 120 125
 Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
 130 135 140
 Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
 145 150 155 160
 Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
 165 170 175
 Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
 180 185 190
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
 195 200 205
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
 210 215 220
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
 225 230 235 240
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
 245 250 255
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
 260 265 270
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
 275 280 285
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
 290 295 300
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Ser Leu Pro
 305 310 315 320
 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu

325 330 335
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
 340 345 350
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
 355 360 365
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr
 370 375 380
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp
 385 390 395 400
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu
 405 410 415
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn
 420 425 430
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu
 435 440 445
 Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
 450 455 460
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
 465 470 475 480
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
 485 490 495
 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
 500 505 510
 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
 515 520 525
 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met
 530 535 540
 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
 545 550 555 560
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
 565 570 575
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
 580 585 590
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
 595 600 605
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
 610 615 620
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile

625 630 635 640
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
 645 650 655
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
 660 665 670
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
 675 680 685
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
 690 695 700
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
 705 710 715 720
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
 725 730 735
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
 740 745 750
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
 755 760 765
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
 770 775 780
 His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
 785 790 795 800
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
 805 810 815
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
 820 825 830
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
 835 840 845
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
 850 855 860
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
 865 870 875 880
 His Ile Val Asn

<210> 6
 <211> 13
 <212> DNA
 <213> Homo sapiens

<220>

<221> intron
 <222> (8)..(13)
 <223> First six bases of Y intron

<400> 6
 ccaggtgggc ctc

13

<210> 7
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last seven bases of intron Y

<400> 7
 gcaggtgtcc tgcc

14

<210> 8
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron 1

<400> 8
 aaagagggtg gctg

14

<210> 9
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last 7 bases of Intron 1

<400> 9
 aacagaagcc gagc

14

<210> 10
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron Alpha

<400> 10

IWS
 A1

tgtcaaggtg gatg

14

<210> 11

<211> 14

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron Alpha

<400> 11

ccccaggac aggc

14

<210> 12

<211> 14

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(14)

<223> First 7 bases of Intron Beta

<400> 12

gagccacgtc tcta

14

<210> 13

<211> 14

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron Beta

<400> 13

ggggcaagtc ctac

14

<210> 14

<211> 14

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(14)

<223> First 7 base of Intron 2

<400> 14

actccaggtg agcg

14

<210> 15

<211> 14

<212> DNA

SW
14

<213> Homo sapiens

<220>

<221> modified base

<222> (1)..(7)

<223> Wherein N is any nucleotide

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron 2

<400> 15

nnnnnnncta tgcc

14

<210> 16

<211> 173

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(166)

<223> Full Sequence of Intron 3

<400> 16

aacgcagccg aagaaaacat ttctgtcgtg actcctgcgg tgcttgggtc gggacagcca 60
gagatggagc caccgcgag accgtcgggt gtgggcagct ttccggtgtc tcctgggagg 120
ggagttgggc tgggcctgtg actcctcagc ctctgttttc cccagggat gtc 173

<210> 17

<211> 46

<212> PRT

<213> Homo sapiens

<400> 17

Thr Ala Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
1 5 10 15

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
20 25 30

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
35 40 45

<210> 18

<211> 104

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Y

<400> 18

ggctccccg ggtcggcgt ccggctgggg ttgagggcgg ccggggggaa ccagcgacat 60
gcggagagca gcgcaggcga ctccaggcgc ttccccgcga ggtg 104

<210> 19
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reding Frame One of Intron Y

<400> 19
 Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly
 1 5 10 15
 Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro
 20 25 30

Arg Arg

<210> 20
 <211> 10
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reading Frame Two of Intron Y before termination
 Codon

<400> 20
 Ala Ser Pro Gly Ser Ala Ser Gly Trp Gly
 1 5 10

<210> 21
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reading Frame Two of Intron Y after termination
 Codon

<400> 21
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly
 20

<210> 22
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>

<223> Reading Frame Three of Intron Y

<400> 22

Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu
1 5 10 15

Pro Ala Thr Cys Gly Glu Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro
20 25 30

Gln Val

<210> 23

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<223> Intron 1

<400> 23

gtggctgtgc tttggtttta cttccttttt aaccagaa

38

<210> 24

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 1 Translation

<400> 24

Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys
1 5 10

<210> 25

<211> 36

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Alpha

<400> 25

gtggatgtga cgggcgcgta cgacaccatc ccccag

36

<210> 26

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<223> Intron Alpha Translation

<400> 26

Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln
 1 5 10

<210> 27
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Intron Beta

<400> 27
 gtctctacct tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag 60
 accagcccgc tgagggatgc cgtcgtcatc gacgacagct cctccctgaa tgaggccagc 120
 agtggcctct tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc 180
 aa 182

<210> 28
 <211> 61
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Intron Beta Translation

<400> 28
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 1 5 10 15
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 20 25 30
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 35 40 45
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 50 55 60

<210> 29
 <211> 226
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Intron 2

<400> 29
 gtgagcgcac ctggccggaa gtggagcctg tgcccggctg gggcagggtgc tgcctgcaggg 60
 ccgttgctgc cacctctgct tccgtgtggg gcaggcgact gccaatccca aagggtcaga 120
 tgccacaggg tgcccctcgt cccatctggg gctgagcaca aatgcattct tctgtgggag 180
 tgagggtgcc tcacaacggg agcagttttc tgtgctattt tggtaa 226

<210> 30
 <211> 159
 <212> DNA

<213> Homo sapiens

<220>

<223> Intron 3

<400> 30

ccgaagaaaa catttctgtc gtgactcctg cgggtgcttg gtcgggacag ccagagatgg 60
agccaccccg cagaccgtcg ggtgtgggca gctttccggt gtctcctggg aggggagttg 120
ggctgggcct gtgactcctc agcctctgtt ttccccag 159

<210> 31

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 3 Translation

<400> 31

Ala Glu Glu Asn Ile Ser Val Val Thr Pro Ala Val Leu Gly Ser Gly
1 5 10 15

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
20 25 30

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
35 40

<210> 32

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<223> Intron X. Complete length unknown

<400> 32

gacagtcacc agggggggttg accgcgggac tgggcgtccc cagggttgac tataggacca 60
ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gtctggctgg catgggtgga 120
cgtggccccc ggcatggcct tctgcgtgtg ctgccgtggg tgccctgagc cctcactgag 180
tcggtggggg cttgtggctt cccgtgagct tccccctagt ctgttgtctg gctgagcaag 240
cctcctgagg ggctctctat tg 262

<210> 33

<211> 218

<212> DNA

<213> Homo sapiens

<220>

<223> Partial Sequence of Genomic Intron (approximately
2.7 kb)

<400> 33

gtggctgtgc tttggtttaa cttccttttt aaccagaagt gcgtttgagc cccacatttg 60
gtatcagctt agatgaaggg ccggaggag gggccacggg acacagccag ggccatggga 120
cggcgcccac ccatttgtgc gcacagttag gtggccgagg tgccggtgcc tccagaaaag 180

cagcctgggg gtgtaggggg agctcctggg gcagggac

218

<210> 34

<211> 2031

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1767)..(1769)

<223> Wherein N is A, C, G or T

<220>

<223> N-Terminal Truncated Telomerase

<400> 34

atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggttct ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gaegcacggc cccccccg cgcctccctc ttccgccagg tgcctgcct gaaggagctg 240
gtggcccagag tgctgcagag gctgtgcgag cgcggcgcca agaactgtgt ggcttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacgtt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420
ctgcgcgcgc tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgt 540
gccactcagg cccggccccc gccatcagct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtcccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgccaagag gccaggcgt 720
ggcgtgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggttcc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttgagggg tgcgtctctt ggcacgcgcc actcccacc atcctgtggc 900
cgccagcacc acgcggggcc cccatccaca tgcggccac cagctccctg ggacacgct 960
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ctgcggccct ccttctact cagctctctg aggccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tgatgccag ggactcccc caggttgccc 1140
cgctgcccc agcgtactg gcaaagtgcg ccctgtttc tggagctgt tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcaactgc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccgaggct ctgtggcggc ccccgaggag 1320
gaggacacag accccgctc cctggtgcag ctgctcgcgc cccaggcct ctggggctcc 1440
gtgtacggct tcgtgcgggc ctgectgcgc cggctggtgc cccaggcct ctggggctcc 1440
aggcacaacg aacgcgcctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtg aagatgagc tgccgggactg cgcttggtg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tctgcactg gctgatgagt gtgtacgtcg tgcagctgt caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggtctt ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaaatnng acagtcacca ggggggttga ccgccgact 1800
ggcgctcccc aggggtgact ataggaccag gtgtccagg gcccgtgcaag tagaggggct 1860
ctcagaggcg tctggctggc atgggtggac gtggccccg gcattgcctt ctgcgtgtgc 1920
tgccgtgggt gccctgagcc ctactgagt cgggtggggc ttgtgcttc ccgtgagctt 1980
ccccctagtc tgttgtctgg ctgagcaagc ctctgaggg gctctctatt g 2031

<210> 35

<211> 588

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Predicted by SEQ ID NO:34

<400> 35

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 580 585

<210> 36
 <211> 2041
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1; Intron 1 Addition

<400> 36

atgccgcgcg ctecccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
 cgcggggacc cggcggtttt ccgcgcgtg gtggcccagt gcctggtgtg cgtgccctgg 180
 gacgcacggc cgcggggcgc cgcggggcgc ttccgccagg tgcctgcct gaaggagctg 240
 gtggcccagag tgcctgcagag gctgtgcgag cgcgggcgca agaactgtgt ggcttcggc 300
 ttccgcgtgc tggacggggc ccgcgggggc ccccccagg ccttcaccac cagcgtgcgc 360
 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420
 ctgcgcgcgc tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
 ctggtggctc ccagctgcgc ctaccaggtg tgcggggcgc cgctgtacca gctcggcgct 540
 gccactcagg cccggggccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
 cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
 gcgaggaggc gcgggggcag tgcagcga agtctgccgt tgccaagag gccaggcgt 720
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 aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
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<210> 37
 <211> 670
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1; Encoded by SEQ ID NO:36

<400> 37

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 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
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 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe
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Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
660 665 670

<210> 38
<211> 2541
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein 2; Alpha Intron Addition

<400> 38

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gaagacagtg gtgaacttcc c 2541

<210> 39

<211> 806

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2; Encoded by SEQ ID NO:38

<400> 39

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35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser Val Leu Arg Pro Val Pro Gly
 755 760 765
 Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu
 770 775 780
 Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala
 785 790 795 800
 Ala Pro Ala Phe Val Gly
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<211> 3396

<212> DNA

<213> Homo sapiens

<220>

<223> Reference Telomerase; with Intron Alpha and Beta

<400> 40

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<210> 41

<211> 3069

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 3; with Introns Alpha, Beta and 2

<400> 41

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<210> 42

<211> 948

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3; Encoded by SEQ ID NO:41

<400> 42

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 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
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 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
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 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
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 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
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 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
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 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
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Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
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 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
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 595 600 605
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 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
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 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
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 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
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 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
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 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
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Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Arg
945

<210> 43

<211> 3362

<212> DNA

<213> Homo sapiens

<220>

<223> Altered C-terminus Protein; with Intron Alpha,
Beta and 3

<400> 43

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<210> 44
 <211> 1096
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Altered C-terminus Protein; Encoded by SEQ ID
 NO:43

<400> 44
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 35 40 45
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 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
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 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
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 545 550 555 560
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 565 570 575
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 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
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 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
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 755 760 765
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 770 775 780
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 785 790 795 800
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 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
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 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
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Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
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 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
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 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
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 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
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 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
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 1045 1050 1055
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 1075 1080 1085
 Gly Arg Gly Val Gly Leu Gly Leu
 1090 1095

<210> 45
 <211> 3918
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Protein that lacks Motif A; with Intron Beta

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 ctccgcttca tccccagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
 ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
 ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gctcctggg cgcctctgtg 2040
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 gaccgcgcgc ctgagctgta ctttgtcaag gacaggtcga cggaggtcat cgcagcatc 2160
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 cagggctcca tctctccac gctgctctgc agcctgtgct acggcgacat ggagaacaag 2520
 ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt tgggtgatga tttctgttg 2580
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 gagtatgct gcgtggtgaa cttgcggaag acagtggga acttccctgt agaagacgag 2700
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 ctgtgccacc aagcattcct gctcaagctg actcgacacc gtgtcaccta cgtgccactc 3240
 ctggggtcac tcaggacagc ccagacgcag ctgagtcgga agctcccggg gacgacgtg 3300
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 cctcctttt cttccaccc ccaccatcca ggtggagacc ctgagaagga ccctgggagc 3780
 tctgggaatt tggagtgacc aaaggtgtgc cctgtacaca ggcgaggacc ctgcacctgg 3840
 atgggggtcc ctgtgggtca aattgggggg aggtgctgtg ggagtaaaat actgaatata 3900
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<210> 46
 <211> 1120
 <212> PRT

<213> Homo sapiens

<220>

<223> Protein that lacks Motif A; Encoded by SEQ ID
NO:45

<400> 46

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 705 710 715 720
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 725 730 735
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 740 745 750
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 755 760 765
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 770 775 780
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 785 790 795 800
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 805 810 815
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 820 825 830
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 835 840 845
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 850 855 860
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 865 870 875 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 885 890 895
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 900 905 910
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 915 920 925
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 930 935 940
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 945 950 955 960
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 965 970 975
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 980 985 990
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 995 1000 1005
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1010 1015 1020
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1025 1030 1035 1040
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1045 1050 1055
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1060 1065 1070
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1075 1080 1085
 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
 1090 1095 1100
 Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1105 1110 1115 1120

<210> 47
 <211> 3033
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein that lacks Motif A; with Introns

Beta and 2

<400> 47

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cgcggggacc	cggcggttt	ccgcgcgtg	gtggcccagt	gcctggtgtg	cgtagccctg	180
gacgcacggc	cgcgcgcgc	cgccccctcc	ttccgccagg	tgtcctgcct	gaaggagctg	240
gtggcccag	tgtgcagag	gctgtgcgag	cgcggcgoga	agaacgtgct	ggccttcggc	300
ttcgcgctgc	tggacggggc	ccgcgggggc	ccccccgagg	ccttcaccac	cagcgtgcgc	360
agctacctgc	ccaacacggt	gaccgacgca	ctgcggggga	gcggggcgtg	ggggctgctg	420
ctgcgcgcgc	tgggcgacga	cgtagctggt	cacctgctgg	cacgctgcgc	gctctttgtg	480
ctggtggctc	ccagctgcgc	ctaccaggtg	tgcgggccc	cgctgtacca	gctcggcgct	540
gccactcagg	ccgggcccc	gccacacgct	agtggacccc	gaaggcgtct	gggatgcgaa	600
cgggcctgga	accatagcgt	cagggaggcc	gggggtcccc	tgggcctgcc	agccccgggt	660
gcgaggaggc	gcgggggag	tgccagccga	agtctgcctg	tgcccaagag	gcccaggcgt	720
ggcgtgccc	ctgagcggga	gcggacgccc	gttgggcagg	ggtcctgggc	ccaccggggc	780
aggacgcgtg	gaccgagtga	ccgtggtttc	tgtgtggtgt	cacctgccag	acccgccgaa	840
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cgcagcacc	acgcggggcc	cccatccaca	tgcggccac	cacgtccctg	ggacacgcct	960
tgtccccggt	tgtacgccga	gaccaagcac	ttcctctact	cctcaggcga	caaggagcag	1020
ctgcggccct	ccttctact	cagctctctg	aggcccagcc	tgactggcgc	tcggaggctc	1080
gtggagacca	tctttctggg	ttccaggccc	tggatgccag	ggactcccc	caggttgccc	1140
cgcctgcccc	agcgtactag	gcaaatgcgg	cccctgtttc	tggagctgct	tgggaaccac	1200
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gccaagctct	cgctgcagga	gctgacgtgg	agatgagcg	tgcgggactg	cgcttggtcg	1560
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ctgtcggag	cagaggtcag	gcagcatcgg	gaagccaggc	ccgcctgct	gacgtccaga	1860
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ggagccagaa	cgttccgcag	agaaaagagg	gccgagcgtc	tcacctcgag	ggtgaaggca	1980
ctgttcagcg	tgtcaacta	cgagcgggcg	cgccgccccg	gcctcctggg	cgcctctgtg	2040
ctgggcctgg	acgatatacca	cagggcctgg	cgcacctcgc	tgtgcgtgt	gcgggcccag	2100
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atgcgacagt	tcgtggctca	cctgcaggag	accagccgc	tgagggatgc	cgctgtcacc	2340
gagcagagct	cctccctgaa	tgaggccagc	agtggcctct	tcgacgtctt	cctacgcttc	2400
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cagggtcca	tctctccac	gctgctctgc	agcctgtgct	acggcgacat	ggagaacaag	2520
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ctctgcttcc	gtgtggggca	ggcgactgcc	aatcccaag	ggtcagatgc	cacagggtgc	2940
ccctcgctcc	atctggggct	gagcacaat	gcattcttct	gtgggagtga	gggtgcctca	3000
caacgggagc	agttttctgt	gctatttttg	taa			3033

<210> 48

<211> 936

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein that lacks Motif A; Encoded by
SEQ ID NO:47

<400> 48

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val

260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr

565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 705 710 715 720
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 725 730 735
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 740 745 750
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 755 760 765
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 770 775 780
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 785 790 795 800
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 805 810 815
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 820 825 830
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 835 840 845
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 850 855 860
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro

865 870 875 880
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 885 890 895
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 900 905 910
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 915 920 925
 Glu Val Gln Ser Asp Tyr Ser Arg
 930 935

<210> 49

<211> 3326

<212> DNA

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus;
 with Introns Beta and 3

<400> 49

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 gccaaagctc cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggtg 1560
 cgcaggagcc caggggttgg ctgtgtcccg gccgcagagc accgtctgcg tgaggagatc 1620
 ctggccaagt tctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
 ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctacc gaagagtgtc 1740
 tggagcaagt tgcaagcat tggaatcaga cagcacttga agaggggtga gctgcgggag 1800
 ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgcctgct gacgtccaga 1860
 ctccgcttca tccccaaagg tgacgggctg cggccgattg tgaacatgga ctacgtgctg 1920

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ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggccag 2100
gaccgcgcgc ctgagctgta ctttgtcaag gacaggctca cggaggtcat cgccagcatc 2160
atcaaacccc agaacacgta ctgcgtgcgt cggatgcccg tgggccagaa ggccgcccac 2220
gggcaagtcg gcaaggcctt caagagccac gtctctacct tgacagacct ccagccgtac 2280
atgcgacagt tcgtggctca cctgcaggag accagcccgc tgagggatgc cgtcgtcatc 2340
gagcagagct cctccctgaa tgaggccagc agtggcctct tcgacgtctt cctacgcttc 2400
atgtgccacc acgccgtgcg catcaggggc aagtcctacg tccagtgccg ggggatcccg 2460
cagggctcca tcctctccac gctgctctgc agcctgtgct acggcgacat ggagaacaag 2520
ctgtttgcgg ggattcggcg ggacgggctg ctctctgctt tggatgatga tttcttgttg 2580
gtgacacccc acctcaccca cgcgaaaacc ttctcagga cctgggtccg aggtgtccct 2640
gagtatggct ggggtgggaa cttgcggaag acagtgggta acttcctgtt agaagacgag 2700
gccctgggtg gcacggcttt tgttcagatg ccggcccacg gcctattccc ctggtgcggc 2760
ctgctgctgg ataccgggac cctggagggtg cagagcgact actccagcta tgcccggacc 2820
tccatcagag ccagctctac ctccaaccgc ggcttcaagg ctgggaggaa catgcgtcgc 2880
aaactctttg gggctctgcg gctgaagtgt cacagcctgt ttctggattt gcaggtgaac 2940
agcctccaga cgggtgtgac caacatctac aagatcctcc tgctgcaggc gtacagggtt 3000
cacgcatgtg tgctgcagct cccatttcat cagcaagttt ggaagaacct cacatttttc 3060
ctgcgcgtca tctctgacac ggctcctctc tgctactcca tcctgaaagc caagaacgca 3120
gccgaagaaa acatttctgt cgtgactcct gcggtgcttg ggtcgggaca gccagagatg 3180
gagccacccc gcagaccgtc ggggtgtggc agctttccgg tgtctcctgg gaggggagtt 3240
gggctggggc tgtgactcct cagcctctgt ttccccccag ggatgtcgct gggggccaag 3300
ggcgccgcgc gccctctgcc ctccga 3326

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<210> 50
 <211> 1084
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus;
 Encoded by SEQ ID NO:49

<400> 50
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

115	120	125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val 130 135 140		
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val 145 150 155 160		
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr 165 170 175		
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly 180 185 190		
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg 195 200 205		
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg 210 215 220		
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg 225 230 235 240		
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp 245 250 255		
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val 260 265 270		
Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala 275 280 285		
Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 295 300		
Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro 305 310 315 320		
Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325 330 335		
Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 340 345 350		
Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 355 360 365		
Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln 370 375 380		
Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 385 390 395 400		
Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg 405 410 415		
Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln		

420	425	430
Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu 435 440 445		
Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe 450 455 460		
Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser 465 470 475 480		
Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser 485 490 495		
Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met 500 505 510		
Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys 515 520 525		
Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe 530 535 540		
Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe 545 550 555 560		
Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr 565 570 575		
Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His 580 585 590		
Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln 595 600 605		
His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile 610 615 620		
Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val 625 630 635 640		
Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser 645 650 655		
Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg 660 665 670		
Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg 675 680 685		
Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro 690 695 700		
Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile 705 710 715 720		
Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln		

725								730				735			
Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser
740								745				750			
Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu
755								760				765			
Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser
770				775								780			
Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe
785				790								795			
Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys
				805								810			
Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu
				820								825			
Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp
835								840				845			
Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His
850				855								860			
Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro
865				870								875			
Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro
				885				890				895			
Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala
				900				905				910			
His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu
915								920				925			
Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala
930				935								940			
Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg
945				950				955				960			
Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp
				965				970				975			
Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile
				980				985				990			
Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro
995								1000				1005			
Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile
1010				1015								1020			
Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	Asn	Ala

1025 1030 1035 1040
 Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly
 1045 1050 1055
 Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
 1060 1065 1070
 Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1075 1080

<210> 51
 <211> 2135
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1871)..(1873)
 <223> Wherein N is A, C, G or T

<220>
 <223> N-Terminal Truncated Telomerase (ver. 2); with
 Intron Y

<400> 51
 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgcccg tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
 gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgccaaca 480
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgctggggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
 gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgctgccact caggcccgcg 660
 ccccgccaca cgetagtga ccccgaggc gtctgggatg cgaacgggcc tggaccata 720
 gcgtcaggga ggccggggtc cccctgggccc tgccagcccc gggcgcgagg aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gccctgagc 840
 cggagcggac gccggttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgccactccc acccatccgt gggccgcccag caccacgcgg 1020
 gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcacttctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
 tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgctg cccagcgct 1260
 actggcaaat gcggccccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
 ggggtgctct caagacgcac tgcccgtgcg gagctgcggt caccaccagca gccggtgtct 1380
 gtgcccgggg gaagccccag ggctctgtgg cgcccccgga ggaggaggac acagaccccc 1440
 gtcgctggtg gcagctgtc cgccagcaca gcagccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgect gcgcgggctg gtgccccag cctctgggg ctccaggcac aacgaacgcc 1560
 gcttctcag gaacaccaag aagttcatct cctggggaa gcatgccaaag ctctcgctgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgca gagcaccgtc tgctgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800

ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat nnngacagtc accagggggg ttgaccgccg gactgggagt cccaggggtt 1920
gactatagga ccaggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980
tgccatgggt ggacgtggcc cggggcatgg ccttctgcgt gtgctgccgt gggtgccctg 2040
agccctcact gagtcggtgg gggcttgtgg cttcccgtga gcttccccct agtctgttgt 2100
ctggctgagc aagcctcctg aggggtcttc tattg 2135

<210> 52

<211> 622

<212> PRT

<213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver.2); encoded
by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala

210	215	220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 225 230 235 240		
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 245 250 255		
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 270		
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 275 280 285		
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 300		
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 310 315 320		
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 335		
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 340 345 350		
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 355 360 365		
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 370 375 380		
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 385 390 395 400		
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 415		
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 430		
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 435 440 445		
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 455 460		
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 465 470 475 480		
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 485 490 495		
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 500 505 510		
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		

515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 610 615 620

<210> 53

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<223> Splicing Variant of Human Telomerase encoded by
 Intron Y, ORF2, before the termination codon.
 SEQ ID NOS: 51,55,59,63,67,71,75,79,83 encode this
 fragment

<400> 53

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala
 65 70 75 80
 Ser Gly Trp Gly

<210> 54

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver. 2); encoded
by SEQ ID NO:51, with Y intron, ORF2, after the
termination codon

<400> 54

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly
 530 535

<210> 55
 <211> 2145
 <212> DNA
 <213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); with Introns Y and 1

<400> 55

```

atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgcccg tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgccctgg 180
gacgcacggc cgcggccgac cgccccctcc ttcggccagg tgggcctccc cggggctcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtctg 360
agaggctgtg cgagcgcggc gcgaagaacg tcttgccctt cggcttcgcg ctgctggacg 420
ggcccccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccacaa 480
cggtgaccga cgcactgcgg gggagcgggg cgtggggggt gctgctgcgc cgcgtgggag 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgcccact caggccccgc 660
ccccgccaca cgctagtggg ccccgagggc gtctgggatg cgaacggggc tggaccata 720
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gcagtgcagc ccgaagtctg ccgttgccca agaggccag gcgtggcgct gcccctgagc 840
cggagcggac gcccggtggg caggggtcct gggccacccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
aggtgtcgct ctctggcacg cgcactccc acccatccgt gggccgccag caccacgcgg 1020
gcccccatc cacatcgcg ccaccacgtc cctgggacac gcctgtccc ccggtgtacg 1080
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tactcagctc tctgaggccc agcctgactg gcgctcgag gctcgtggag accatctttc 1200
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<210> 56

<211> 704

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); encoded by SEQ ID
NO:55, with Y Intron ORF1

<400> 56

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
      20           25           30

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Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	
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65						70						75			80	
Val	Arg	Leu	Gly	Leu	Arg	Ala	Ala	Gly	Gly	Asn	Gln	Arg	His	Ala	Glu	
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Ser	Ser	Ala	Gly	Asp	Ser	Gly	Arg	Phe	Pro	Arg	Arg	Ser	Cys	Leu	Lys	
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Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	
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Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	
130						135						140				
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Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	
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Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	
			180						185						190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	
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Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	
210						215						220				
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	
225						230						235			240	
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	
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Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	
			260						265						270	
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	
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Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	
290						295						300				
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	
305						310						315			320	
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	
			325						330						335	

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu
 675 680 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
 690 695 700

<210> 57

<211> 619

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2): encoded by SEQ ID
 NO:55, with Intron Y ORF2 after the termination
 codon

<400> 57

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590

Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu
 595 600 605

Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
 610 615

<210> 58

<211> 704

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); encoded by SEQ ID
 NO:55, with Intron Y ORF3

<400> 58

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu

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Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys						
			100					105					110								
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys						
		115					120					125									
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly						
	130					135					140										
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr						
145					150					155					160						
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg						
				165					170					175							
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu						
			180					185					190								
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro						
		195					200					205									
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala						
	210					215					220										
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser						
225					230					235					240						
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg						
				245					250					255							
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro						
			260					265					270								
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly						
		275					280					285									
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe						
	290					295					300										
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu						
305					310					315					320						
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln						
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Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser						
		355																			

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 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
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 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu
 675 680 685
 Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly

690

695

700

<210> 59
 <211> 2645

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); with Intron Y and Alpha

<400> 59

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gtggatgatt tcttggttgg gacacctcac ctcacccacg cgaaaacctt cctcaggacc 2580
ctgggtccgag gtgtccctga gtatggctgc gtggtgaact tgcggaagac agtgggtgaac 2640
ttccc                                           2645

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<210> 60
 <211> 841
 <212> PRT
 <213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID
 NO:59, with Intron Y ORF1

<400> 60

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      20              25              30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
    35              40              45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50              55              60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
   65              70              75              80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
      85              90              95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
    100              105              110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
    115              120              125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130              135              140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
   145              150              155              160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
    165              170              175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
    180              185              190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
    195              200              205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210              215              220

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Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
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 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro
 785 790 795 800
 Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln
 805 810 815
 Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala
 820 825 830

Gly Arg Ala Ala Pro Ala Phe Val Gly
835 840

<210> 61
<211> 756
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID
NO:59 with Intron Y ORF2 after the termination
codon

<400> 61
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30
Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45
Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60
Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80
Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95
Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110
Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125
Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140
Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160
Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175
Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190
Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205
Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro
 705 710 715 720
 Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
 725 730 735
 His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
 740 745 750
 Ala Phe Val Gly
 755

<210> 62
 <211> 841
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:
 59 with Intron Y ORF3

<400> 62
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly	20	25	30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg	35	40	45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro	50	55	60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg	65	70	75
Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu	85	90	95
Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys	100	105	110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys	115	120	125
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly	130	135	140
Pro Pro Glu Ala Phe Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr	145	150	155
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg	165	170	175
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu	180	185	190
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro	195	200	205
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala	210	215	220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser	225	230	235
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg	245	250	255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro	260	265	270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly	275	280	285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe	290	295	300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu			

305		310		315		320
Gly Ala Leu Ser	Gly Thr Arg His Ser	His Pro Ser Val	Gly Arg Gln			
	325	330	335			
His His Ala Gly	Pro Pro Ser Thr	Ser Arg Pro Pro Arg	Pro Trp Asp			
	340	345	350			
Thr Pro Cys Pro	Pro Val Tyr	Ala Glu Thr Lys	His Phe Leu Tyr Ser			
	355	360	365			
Ser Gly Asp Lys	Glu Gln Leu Arg	Pro Ser Phe	Leu Leu Ser Ser Leu			
	370	375	380			
Arg Pro Ser Leu	Thr Gly Ala Arg Arg	Leu Val Glu Thr	Ile Phe Leu			
	385	390	395			400
Gly Ser Arg Pro	Trp Met Pro Gly Thr	Pro Arg Arg Leu	Pro Arg Leu			
	405	410	415			
Pro Gln Arg Tyr	Trp Gln Met Arg	Pro Leu Phe Leu	Glu Leu Leu Gly			
	420	425	430			
Asn His Ala Gln	Cys Pro Tyr Gly	Val Leu Leu Lys	Thr His Cys Pro			
	435	440	445			
Leu Arg Ala Ala	Val Thr Pro Ala Ala	Gly Val Cys Ala	Arg Glu Lys			
	450	455	460			
Pro Gln Gly Ser	Val Ala Ala Pro	Glu Glu Glu Asp	Thr Asp Pro Arg			
	465	470	475			480
Arg Leu Val Gln	Leu Leu Arg Gln	His Ser Ser Pro	Trp Gln Val Tyr			
	485	490	495			
Gly Phe Val Arg	Ala Cys Leu Arg	Arg Leu Val Pro	Pro Gly Leu Trp			
	500	505	510			
Gly Ser Arg His	Asn Glu Arg Arg	Phe Leu Arg Asn	Thr Lys Lys Phe			
	515	520	525			
Ile Ser Leu Gly	Lys His Ala Lys	Leu Ser Leu Gln	Glu Leu Thr Trp			
	530	535	540			
Lys Met Ser Val	Arg Asp Cys Ala	Trp Leu Arg Arg	Ser Pro Gly Val			
	545	550	555			560
Gly Cys Val Pro	Ala Ala Glu His	Arg Leu Arg Glu	Glu Ile Leu Ala			
	565	570	575			
Lys Phe Leu His	Trp Leu Met Ser	Val Tyr Val Val	Glu Leu Leu Arg			
	580	585	590			
Ser Phe Phe Tyr	Val Thr Glu Thr	Thr Phe Gln Lys	Asn Arg Leu Phe			
	595	600	605			
Phe Tyr Arg Lys	Ser Val Trp Ser	Lys Leu Gln Ser	Ile Gly Ile Arg			

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<210> 63
<211> 3500
<212> DNA
<213> Homo sapiens

<220>
<223> Reference Protein (ver.2); with Introns Y, Alpha
      and Beta

<400> 63
atgccgcgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
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<220>
<223> Reference Protein (ver.2); with Introns Y, Alpha
and Beta

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<400> 63
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
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cgcggggacc	cgcgggcttt	cgcgcgctg	gtggcccagt	gcctggtgtg	cgtgccectg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggcctccc	cggggtcggc	240
gtccggctgg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctggtggcc	cgagtgtgc	360
agaggctgtg	cgagcgcggc	gcgaagaacg	tgtggcctt	cggettcgcg	ctgctggacg	420
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gcgcctacca	ggtgtgcggg	cgcccgctgt	accagctcgg	cgctgccact	caggcccggc	660
ccccgccaca	cgctagtggg	ccccgaaggc	gtctgggatg	cgaacggggc	tggaaccata	720
gcgtcagggg	ggccgggggt	cccctggggc	tgccagcccc	gggtgcgagg	aggcgcgggg	780
gcagtgccag	ccgaagtctg	ccgttgccca	agaggcccag	gcgtggcgct	gcccctgagc	840
cggagcggac	gcccgttggg	cagggttcct	gggcccaccc	gggcaggacg	cgtggaccga	900
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tggtccagaa	ggccgcccac	gggcacgtcc	gcaaggcctt	caagagccac	gtctctacct	2400
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ttctggattt	gcaggtgaac	agcctccaga	cgggtgtgcac	caacatctac	aagatcctcc	3120
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ggaagaaccc	cacatttttc	ctgcgcgtca	tctctgacac	ggcctccctc	tgtactcca	3240
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gtgtcaccta	cgtgccactc	ctgggggtcac	tcaggacagc	ccagacgcag	ctgagtcgga	3420
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<210> 64
 <211> 1165
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF1

<400> 64

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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35           40           45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50           55           60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65           70           75           80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85           90           95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100           105           110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115           120           125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130           135           140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145           150           155           160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165           170           175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180           185           190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195           200           205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210           215           220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225           230           235           240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

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245										250					255				
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro				
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Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly				
		275					280					285							
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe				
	290					295					300								
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu				
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Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln				
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His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp				
		340						345					350						
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser				
		355					360					365							
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu				
	370					375					380								
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu				
385					390				395						400				
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu				
				405					410					415					
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly				
		420						425					430						
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro				
		435					440					445							
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys				
	450					455					460								
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg				
465					470				475					480					
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr				
				485				490						495					
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp				
		500						505					510						
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe				
		515					520					525							
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp				
	530					535					540								
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val				

545		550		555		560
Gly Cys Val Pro	Ala Ala Glu His Arg	Leu Arg Glu Glu Ile	Leu Ala			
	565	570	575			
Lys Phe Leu His	Trp Leu Met Ser Val Tyr Val Val	Glu Leu Leu Arg				
	580	585	590			
Ser Phe Phe Tyr	Val Thr Glu Thr Thr Phe Gln Lys	Asn Arg Leu Phe				
	595	600	605			
Phe Tyr Arg Lys	Ser Val Trp Ser Lys Leu Gln Ser	Ile Gly Ile Arg				
	610	615	620			
Gln His Leu Lys	Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu	Val				
	625	630	635			640
Arg Gln His Arg	Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg	Leu Arg				
	645	650	655			
Phe Ile Pro Lys	Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr					
	660	665	670			
Val Val Gly Ala	Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu					
	675	680	685			
Thr Ser Arg Val	Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala					
	690	695	700			
Arg Arg Pro Gly	Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile					
	705	710	715			720
His Arg Ala Trp	Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro					
	725	730	735			
Pro Pro Glu Leu	Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp					
	740	745	750			
Thr Ile Pro Gln	Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys					
	755	760	765			
Pro Gln Asn Thr	Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala					
	770	775	780			
Ala His Gly His	Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu					
	785	790	795			800
Thr Asp Leu Gln	Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu					
	805	810	815			
Thr Ser Pro Leu	Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu					
	820	825	830			
Asn Glu Ala Ser	Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys					
	835	840	845			
His His Ala Val	Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly					

850	855	860
Ile Pro Gln Gly Ser	Ile Leu Ser Thr	Leu Leu Cys Ser Leu Cys Tyr
865	870	875 880
Gly Asp Met Glu Asn Lys	Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu	
	885	890 895
Leu Leu Arg Leu Val Asp Asp Phe	Leu Leu Val Thr Pro His Leu Thr	
	900	905 910
His Ala Lys Thr Phe Leu Arg Thr	Leu Val Arg Gly Val Pro Glu Tyr	
	915	920 925
Gly Cys Val Val Asn Leu Arg Lys Thr	Val Val Asn Phe Pro Val Glu	
	930	935 940
Asp Glu Ala Leu Gly Gly Thr Ala Phe Val	Gln Met Pro Ala His Gly	
	945	950 955 960
Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val		
	965	970 975
Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu		
	980	985 990
Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu		
	995	1000 1005
Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln		
	1010	1015 1020
Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu		
	1025	1030 1035 1040
Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His		
	1045	1050 1055
Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp		
	1060	1065 1070
Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser		
	1075	1080 1085
Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln		
	1090	1095 1100
Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val		
	1105	1110 1115 1120
Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu		
	1125	1130 1135
Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala		
	1140	1145 1150
Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp		

1155

1160

1165

<210> 65
 <211> 1081
 <212> PRT
 <213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF2 after the termination codon

<400> 65

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15
 Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30
 Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720
 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
 900 905 910
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
 915 920 925
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
 930 935 940
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
 945 950 955 960
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
 965 970 975
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
 980 985 990
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys
 995 1000 1005
 Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His
 1010 1015 1020
 Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro
 1025 1030 1035 1040
 Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu
 1045 1050 1055
 Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu
 1060 1065 1070
 Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1075 1080

<210> 66
 <211> 1165
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF3

<400> 66

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070
 Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
 1075 1080 1085
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
 1090 1095 1100
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
 1105 1110 1115 1120
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
 1125 1130 1135
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
 1140 1145 1150
 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1155 1160 1165

<210> 67
 <211> 3173
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein (ver.2); with Introns Y, Alpha,
 Beta and 2

<400> 67

atgccgcg	ctccccgctg	ccgagccgtg	cgctccctgc	tgcgcagcca	ctaccgcgag	60
gtgctgccgc	tggccacgtt	cgtgcggcgc	ctggggcccc	agggctggcg	gctgggtgcag	120
cgccggggacc	cgccggcctt	ccgcgcgctg	gtggcccagt	gcctggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggctctcc	cggggtcggc	240
gtccggttg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctggtggcc	cgagtgtctg	360
agaggctgtg	cgagcgcggc	gcgaagaacg	tgctggcctt	cggcttcgcg	ctgctggacg	420
gggcccgcg	gggccccccc	gaggccttca	ccaccagcgt	gcgcagctac	ctgcccaca	480
cggtgaccga	cgcactgcgg	gggagcgggg	cgtgggggct	gctgctgcgc	cgctggtggc	540
acgacgtgct	ggttcacctg	ctggcacgct	gcgcgctctt	tgtgctggtg	gctcccagct	600
gcgcctacca	ggtgtgcggg	ccgcgcgctg	accagctcgg	cgtgccact	caggcccggc	660
ccccgccaca	cgctagtggg	ccccgaaggc	gtctgggatg	cgaacggggc	tggaaccata	720
gcgtcagggg	ggccgggggtc	cccctggggc	tgccagcccc	gggtgcgagg	aggcgcgggg	780
gcagtgccag	ccgaagtctg	ccgttgccca	agaggccag	gcgtggcgct	gcccctgagc	840
cggagcggac	gcccgttggtg	caggggtcct	gggcccaccc	gggcaggacg	cgtggaccga	900
gtgaccgtgg	tttctgtgtg	gtgtcacctg	ccagaccgcg	cgaagaagcc	acctcttttg	960
aggggtgcgt	ctctggcacg	cgccactccc	accatccgt	gggcccgcag	caccacgcgg	1020
gccccccatc	cacatcgcgg	ccaccacgtc	cctgggacac	gccttgtccc	ccgtgtacg	1080
ccgagaccaa	gcacttccc	tactcctcag	gcgacaagga	gcagctgcgg	ccctccttcc	1140
tactcagctc	tctgaggccc	agcctgactg	gcctcggag	gctcgtggag	accatctttc	1200
tgggttccag	gccctggatg	ccagggaactc	ccgcaggtt	gccccgcctg	cccagcgt	1260
actggcaaat	gcggccccctg	tttctggagc	tgcttgggaa	ccacgcgcag	tgccccctacg	1320
gggtgctcct	caagacgcac	tgcccgcctg	gagctgcggt	caccccagca	gcccgtgtct	1380
gtgcccggga	gaagccccag	ggctctgtgg	cgccccccga	ggaggaggac	acagaccccc	1440
gtgcctggt	gcagctgctc	cgccagcaca	gcagcccctg	gcaggtgtac	ggcttcgtgc	1500
gggctgctg	gcgcgggctg	gtgccccccag	gcctctgggg	ctccaggcac	aacgaacgcc	1560
gcttccctcag	gaacaccaag	aagttcatct	ccctggggaa	gcctgccaag	ctctcgtctg	1620
aggagctgac	gtggaagatg	agcgtgcggg	actgcgctg	gctgcgcagg	agcccagggg	1680
ttggctgtgt	tccggccgca	gagcaccgtc	tgctgagga	gatcctggcc	aagttcctgc	1740
actggctgat	gagtgtgtac	gtcgtcgagc	tgctcaggtc	tttcttttat	gtcacggaga	1800
ccacgtttca	aaagaacagg	ctctttttct	accggaagag	tgtctggagc	aagttgcaaa	1860
gcatttgaat	cagacagcac	ttgaagaggg	tgacgtgcg	ggagctgtcg	gaagcagagg	1920
tcaggcagca	tccgggaagcc	aggcccgcgc	tgctgacgtc	cagactccgc	ttcatcccca	1980
agcctgacgg	gctgcggccg	attgtgaaca	tggactacgt	cgtgggagcc	agaacgttcc	2040
gcagagaaaa	gagggccgag	cgtctcacct	cgagggtgaa	ggcactgttc	agcgtgctca	2100
actacgagcg	ggcgcggcgc	cccggcctcc	tgggcgcctc	tggtgctggg	ctggacgata	2160
tccacagggc	ctggcgcaac	ttcgtgctgc	gtgtgcgggc	ccaggacccg	ccgcctgagc	2220
tgtactttgt	caaggtggat	gtgacgggcg	cgtacgacac	catccccag	gacaggctca	2280
cgaggtcat	cgccagcatc	atcaaaccac	agaacacgta	ctgcgtgcgt	cggtatgccg	2340
tggtccagaa	ggccgcccac	gggcacgtcc	gcaaggcctt	caagagccac	gtctctacct	2400
tgacagacct	ccagccgtac	atgcgacagt	tcgtggtcga	cctgcaggag	accagcccgc	2460
tgagggatgc	cgtcgtcatc	gagcagagct	cctccctgaa	tgaggccagc	agtggcctct	2520
tcgacgtctt	cctacgcttc	atgtgccacc	acgcctgctg	catcaggggc	aagtcctacg	2580
tccagtgcc	gggatcccg	cagggtccca	tcctctccac	gctgctctgc	agcctgtgct	2640
acggcgacat	ggagaacaag	ctgtttgcgg	ggattcggcg	ggacgggctg	ctcctgcgtt	2700
tggtggatga	tttcttggtg	gtgacacctc	acctcaccca	cgcgaaaacc	ttcctcagga	2760
ccctggtccg	aggtgtccct	gagtatggct	gcgtgggtgaa	cttgcggaag	acagtgtgta	2820
acttccctgt	agaagacgag	gccctgggtg	gcacggcttt	tggtcagatg	ccggcccacg	2880
gcctattccc	ctggtgcggc	ctgctgctgg	ataccgggac	cctggagggtg	cagagcgact	2940
actccagggtg	agcgcacctg	gcccgaagtg	gagcctgtgc	ccggctgggg	caggtgctgc	3000
tgcagggccg	ttgcgtccac	ctctgcttcc	gtgtggggca	ggcgactgcc	aatcccaaa	3060
ggtcagatgc	cacaggggtg	ccctcgtccc	atctggggct	gagcacaat	gcctctttct	3120
gtgggagtga	gggtgcctca	caacggggagc	agttttctgt	gctatttttg	ttaa	3173

<210> 68

<211> 982
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF1

<400> 68

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	1	5	10	15
His	Thr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	20	25	30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	35	40	45	
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	50	55	60	
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Gly	Leu	Pro	Gly	Val	Gly	65	70	75	80
Val	Arg	Leu	Gly	Leu	Arg	Ala	Ala	Gly	Gly	Asn	Gln	Arg	His	Ala	Glu	85	90	95	
Ser	Ser	Ala	Gly	Asp	Ser	Gly	Arg	Phe	Pro	Arg	Arg	Ser	Cys	Leu	Lys	100	105	110	
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	115	120	125	
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	130	135	140	
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	145	150	155	160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	165	170	175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	180	185	190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	195	200	205	
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	210	215	220	
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	225	230	235	240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	245	250	255	

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
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Gln Ser Asp Tyr Ser Arg
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<210> 69
 <211> 897
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF2 after the termination
 codon

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
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 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895

Arg

<210> 70

<211> 982

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3 (Ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF3

<400> 70

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

50											55											60			
Pro 65	Pro	Ala	Ala	Pro	Ser 70	Phe	Arg	Gln	Val	Pro 75	Pro	Arg	Gly	Arg	Arg 80										
Pro	Ala	Gly	Val	Glu 85	Gly	Gly	Arg	Gly	Glu 90	Pro	Ala	Thr	Cys	Gly 95	Glu										
Gln	Arg	Arg	Arg 100	Leu	Arg	Ala	Leu	Pro 105	Pro	Gln	Val	Ser	Cys 110	Leu	Lys										
Glu	Leu	Val 115	Ala	Arg	Val	Leu	Gln 120	Arg	Leu	Cys	Glu	Arg 125	Gly	Ala	Lys										
Asn	Val 130	Leu	Ala	Phe	Gly	Phe 135	Ala	Leu	Leu	Asp	Gly 140	Ala	Arg	Gly	Gly										
Pro 145	Pro	Glu	Ala	Phe	Thr 150	Thr	Ser	Val	Arg	Ser 155	Tyr	Leu	Pro	Asn	Thr 160										
Val	Thr	Asp	Ala	Leu 165	Arg	Gly	Ser	Gly	Ala 170	Trp	Gly	Leu	Leu	Leu	Arg										
Arg	Val	Gly	Asp 180	Asp	Val	Leu	Val	His 185	Leu	Leu	Ala	Arg	Cys 190	Ala	Leu										
Phe	Val 195	Leu	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys 205	Gly	Pro	Pro										
Leu	Tyr 210	Gln	Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala										
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240										
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala 255	Arg										
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro										
Arg	Arg	Gly	Ala 275	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly										
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe										
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320										
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln										
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp										
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser										

355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	395
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg		
465	470	475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr		
485	490	495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp		
500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		
515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp		
530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val		
545	550	555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala		
565	570	575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg		
580	585	590
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe		
595	600	605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg		
610	615	620
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val		
625	630	635
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg		
645	650	655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr		

660					665					670					
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu
		675					680					685			
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala
	690					695					700				
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
705				710						715					720
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
				725					730					735	
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp
			740					745					750		
Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys
	755						760					765			
Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala
	770					775					780				
Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu
785				790					795						800
Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu
				805					810					815	
Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu
			820					825					830		
Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys
		835					840					845			
His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly
	850					855					860				
Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr
865						870					875				880
Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu
				885					890					895	
Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr
			900					905					910		
His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr
		915					920					925			
Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu
	930					935					940				
Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly
945				950						955					960
Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val

965

970

975

Gln Ser Asp Tyr Ser Arg
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<210> 71
<211> 3466
<212> DNA
<213> Homo sapiens

<220>
<223> Altered C-Terminus Protein (ver.2); with Introns
Y, Alpha, Beta and 3

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tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag accagcccg 2460

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tgtctcctgg gaggggagtt gggctgggcc tgtgactcct cagcctctgt tttccccag 3420
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<210> 72
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> Altered C-Terminus Protein (ver.2); encoded by SEQ
 ID NO:71 with Intron Y ORF1

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 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
 1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
 1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
 1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1125 1130

<210> 73

<211> 1045

<212> PRT

<213> Homo sapiens

<220>
 <223> Altered C-Terminus Protein (ver.2); encoded by SEQ
 ID NO:71 with Intron Y ORF2 after the termination
 codon

<400> 73
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720
 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
 900 905 910
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
 915 920 925
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
 930 935 940
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
 945 950 955 960
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
 965 970 975
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
 980 985 990
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val
 995 1000 1005
 Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro
 1010 1015 1020
 Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro Gly Arg Gly
 1025 1030 1035 1040
 Val Gly Leu Gly Leu
 1045

<210> 74

<211> 1130

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
ID NO:71 with Intron Y ORF3

<400> 74

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070
 Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
 1075 1080 1085
 Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
 1090 1095 1100
 Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
 1105 1110 1115 1120
 Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1125 1130

<210> 75
 <211> 4022
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); with Introns Y
 and Beta

<400> 75

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cgcggggacc	cggcggcttt	ccgcgcgctg	gtggcccagt	gcctgggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggcctccc	cggggtcggc	240
gtccggctgg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctgggtggc	cgagtgtctg	360
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cggtgaccga	cgcactgcgg	gggagcgggg	cgtgggggct	gctgctgcgc	cgctggggcg	540
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ccaagggcgc	cgccggccct	ctgccctccg	aggccgtgca	gtggctgtgc	caccaagcat	3300

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tcctgctcaa gctgactcga caccgtgtca cctacgtgcc actcctgggg tcactcagga 3360
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<210> 76

<211> 1154

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
NO:75 with Intron Y ORF1

<400> 76

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
      20              25              30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
      35              40              45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
      50              55              60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
      65              70              75              80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
      85              90              95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
      100              105              110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
      115              120              125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
      130              135              140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
      145              150              155              160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
      165              170              175

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Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
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 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780

Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	785	790	795	800
His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	805	810	815	
Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	820	825	830	
Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	835	840	845	
Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	850	855	860	
Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	865	870	875	880
Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	885	890	895	
Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	900	905	910	
Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	915	920	925	
Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	930	935	940	
Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	945	950	955	960
Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	965	970	975	
Arg	Ala	Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	980	985	990	
Arg	Arg	Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	995	1000	1005	
Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	1010	1015	1020	
Lys	Ile	Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	1025	1030	1035	1040
Leu	Pro	Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	1045	1050	1055	
Val	Ile	Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	1060	1065	1070	
Asn	Ala	Gly	Met	Ser	Leu	Gly	Ala	Lys	Gly	Ala	Ala	Gly	Pro	Leu	Pro	1075	1080	1085	

Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu
 1090 1095 1100

Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr
 1105 1110 1115 1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala
 1125 1130 1135

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile
 1140 1145 1150

Leu Asp

<210> 77
 <211> 1069
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
 NO:75 with Intron Y ORF2 after the termination
 codon

<400> 77
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15
 Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30
 Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
 660 665 670
 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
 675 680 685
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
 690 695 700
 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
 705 710 715 720
 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
 725 730 735
 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
 740 745 750
 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
 755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
 770 775 780

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
 785 790 795 800

Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
 805 810 815

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 820 825 830

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
 835 840 845

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 850 855 860

Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
 865 870 875 880

Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
 885 890 895

Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
 900 905 910

Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
 915 920 925

Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
 930 935 940

Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
 945 950 955 960

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
 965 970 975

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
 980 985 990

Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
 995 1000 1005

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
 1010 1015 1020

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
 1025 1030 1035 1040

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
 1045 1050 1055

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1060 1065

<210> 78
 <211> 1154
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
 NO:75 with Intron Y ORF3

<400> 78
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

245																250								255																																	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro																																										
			260																			265																			270																
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly																																										
			275																			280																			285																
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe																																										
			290																			295																			300																
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu																																										
			305																			310																			315																
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln																																										
				325																			330																			335															
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp																																										
			340																			345																			350																
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser																																										
			355																			360																			365																
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu																																										
			370																			375																			380																
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu																																										
			385																			390																			395																
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu																																										
				405																			410																			415															
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly																																										
			420																			425																			430																
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro																																										
			435																			440																			445																
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys																																										
			450																			455																			460																
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg																																										
			465																			470																			475																
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr																																										
				485																			490																			495															
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp																																										
			500																			505																			510																
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe																																										
			515																			520																			525																
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp																																										
			530																			535																			540																
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val																																										

545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys

850	855	860
Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg 865 870 875 880		
Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr 885 890 895		
Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly 900 905 910		
Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn 915 920 925		
Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met 930 935 940		
Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg 945 950 955 960		
Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile 965 970 975		
Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met 980 985 990		
Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe 995 1000 1005		
Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr 1010 1015 1020		
Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln 1025 1030 1035 1040		
Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg 1045 1050 1055		
Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys 1060 1065 1070		
Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro 1075 1080 1085		
Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu 1090 1095 1100		
Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr 1105 1110 1115 1120		
Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala 1125 1130 1135		
Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile 1140 1145 1150		
Leu Asp		

<210> 79
 <211> 3137
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein Lacking Motif A (ver.2); with
 Introns Y, Beta and 2

<400> 79
 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
 cgccggggacc cggcggtttt ccgcgcgtg gtggccaggt gcctgggtgtg cgtgccctgg 180
 gacgcacggc cggccccccg cggccccctc ttccgccagg tgggcctccc cgggggtcggc 240
 gtcgggtgtg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cagtgctgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgcctggcctt cggcttcgcg ctgctggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
 gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgctgccact caggcccggc 660
 ccccgccaca cgctagtga ccccggaagg gtctgggatg cgaacgggccc tggaaaccata 720
 gcgtcaggga ggccgggggt cccctgggccc tgccagcccc ggggtgcagg aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agaggccag gcgtggcgct gccctgagc 840
 cggagcggac gcccggtggg caggggtcct gggccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acctcttgg 960
 aggggtgcgt ctctggcacg cggcactccc acccatccgt gggccgccag caccacgcgg 1020
 gccccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatcttcc 1200
 tgggttccag gccctggatg ccagggactc tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1260
 actggcaaat gcggccccgt tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
 ggggtgctcct caagacgcac tgcccgtgc gagctgcggt caccacagca gccggtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
 gtcgctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgcct gcgcgggtg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttcctcag gaacaccaag aagttcatct ccttggggaa gcatgccaag ctctcgctgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgca gagcacgcgt tgcgtgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
 gcatttgaat cagacagcac ttgaagaggg tgcagctgcg ggaagtgtcg gaagcagagg 1920
 tcaggcagca tcgggaagcc agggccgccc tgcgtacgtc cagactccgc ttcaccccca 1980
 agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaaggttcc 2040
 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
 actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
 tccacagggc ctggcgaccc ttcgtgctgc gtgtgcgggc ccaggaccgc ccgcctgagc 2220
 tgtactttgt caaggacagg ctacgcgag catcatcaaa cccagaaca 2280
 cgtactgcgt gcgtcggtat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340
 ccttcaagag ccacgtctct acctgacag acctccagcc gtacatgcga cagttcgtgg 2400
 ctacactgca ggagaccagc ccgctgagg atgcgctcgt catcgagcag agctcctccc 2460
 tgaatgaggg cagcagtggc ctcttcgacg tcttcctacg ctcatgtgc caccacgcgg 2520
 tgcgcacag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580
 ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctggtt gcggggattc 2640

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ggcggggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
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tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
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ggcaggcgac tgccaatccc aaagggtcag atgccacagg gtgcccctcg tcccatctgg 3060
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ctgtgctatt ttggtaa 3137

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<210> 80

<211> 970

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein lacking Motif A (ver.2); encoded
by SEQ ID NO:79 with Intron Y ORF1

<400> 80

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20           25           30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35           40           45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50           55           60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65           70           75           80
Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85           90           95
Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100           105           110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115           120           125
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130           135           140
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145           150           155           160
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165           170           175
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180           185           190
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

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195					200					205					
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
210						215					220				
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
225					230					235					240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
				245					250					255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
			260					265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
		275					280					285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
290					295					300					
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
305					310					315					320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
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His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
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Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
		355					360					365			
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
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Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu
385					390					395					400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu
				405					410					415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly
			420					425					430		
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro
		435					440					445			
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys
	450					455					460				
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg
465					470					475					480
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr
				485					490					495	
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp

500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 515 520 525		
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 535 540		
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545 550 555 560		
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 570 575		
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580 585 590		
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 600 605		
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 610 615 620		
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 625 630 635 640		
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 655		
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 665 670		
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 675 680 685		
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 690 695 700		
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 705 710 715 720		
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 725 730 735		
Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala 740 745 750		
Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val 755 760 765		
Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His 770 775 780		
Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala 785 790 795 800		
His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln		

65		70		75		80
Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp						
	85			90		95
Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala						
	100			105		110
Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly						
	115			120		125
Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg						
	130			135		140
Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly						
	145			150		155
Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser						
				165		170
Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala						
	180			185		190
Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro						
	195			200		205
Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro						
	210			215		220
Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly						
	225			230		235
Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro						
				245		250
Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro						
	260			265		270
Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu						
	275			280		285
Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr						
	290			295		300
Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp						
	305			310		315
Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp						
				325		330
Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys						
	340			345		350
Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val						
	355			360		365
Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val						

370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
 660 665 670
 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala

675 680 685
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
 690 695 700
 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
 705 710 715 720
 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
 725 730 735
 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
 740 745 750
 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
 755 760 765
 Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
 770 775 780
 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
 785 790 795 800
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
 805 810 815
 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 820 825 830
 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
 835 840 845
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 850 855 860
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
 865 870 875 880
 Ser Asp Tyr Ser Arg
 885

<210> 82
 <211> 970
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein lacking Motif A (ver.2); encoded
 by SEQ ID NO:79 with Intron Y ORF3

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 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg
 965 970

<210> 83
 <211> 3432
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); with Intron Y, Beta and 3

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 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
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 tgtactttgt caaggacagg ctacaggagg tcatcgccag catcatcaaa cccagaaca 2280
 cgtactgcgt gcgtcggtat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340

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cgtcgggtgt gggcagcttt ccggtgtctc ctgggagggg agttgggctg ggctgtgac 3360
tcctcagcct ctgttttccc ccagggatgt cgctgggggc caagggcgcc gccggccctc 3420
tgccctccga ga 3432

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<210> 84
 <211> 1122
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF1

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 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
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 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
 965 970 975
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
 980 985 990
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
 995 1000 1005
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
 1010 1015 1020
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
 1025 1030 1035 1040
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
 1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
 1060 1065 1070

Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
 1075 1080 1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
 1090 1095 1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile
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Gly Ala

<210> 85
 <211> 1037
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF2 after the termination codon

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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
 660 665 670
 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
 675 680 685
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
 690 695 700
 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
 705 710 715 720
 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
 725 730 735
 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
 740 745 750
 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
 755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
 770 775 780
 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
 785 790 795 800
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
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 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 820 825 830
 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
 835 840 845
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 850 855 860
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
 865 870 875 880
 Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
 885 890 895
 Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
 900 905 910
 Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
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 Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
 930 935 940
 Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
 945 950 955 960
 Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
 965 970 975
 Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu
 980 985 990
 Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu
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 1025 1030 1035

<210> 86

<211> 1122

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
(ver.2); encoded by SEQ ID NO:83 with Intron Y
ORF3

<400> 86

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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
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Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
      65           70           75           80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
      85           90           95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
      100          105          110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
      115          120          125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
      130          135          140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
      145          150          155          160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
      165          170          175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
      180          185          190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
      195          200          205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
      210          215          220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
      225          230          235          240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
      245          250          255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
      260          265          270

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Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
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 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
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 835 840 845
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 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
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 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
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 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
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 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
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 Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
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<210> 87

<211> 7615

<212> DNA

<213> Homo sapiens

<220>

<223> Human Telomerase Clone with Exon Beta Spliced Out

<400> 87

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<213> Homo sapiens

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<223> Human Telomerase Clone with exon Alpha Spliced Out

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<400> 90
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<210> 91
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<213> Unknown

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<223> Description of Unknown Organism: Consensus P-loop
      Motif Sequence found in large number of protein
      families

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<222> (2)..(5)
<223> Wherein Xaa is any residue

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<400> 91
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<210> 92
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<212> PRT
<213> Homo sapiens

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<400> 92
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Gly

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<210> 93
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<212> PRT
<213> Unknown

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<220>

<223> Description of Unknown Organism: Consensus c-Alb
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<221> MOD_RES

<222> (2)..(5)

<223> Wherein Xaa is any residue

<220>

<221> MOD_RES

<222> (7)..(8)

<223> Wherein Xaa is any residue

<400> 93

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1 5

<210> 94

<211> 17

<212> PRT

<213> Homo sapiens

<400> 94

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Pro

<210> 95

<211> 14

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: General Target
Sequence Recognized by Hairpin Ribozyme

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<222> (1)..(3)

<223> Wherein N is G, U, C or A

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<221> modified_base

<222> (5)

<223> Wherein N is G, U, C or A

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<221> modified_base

<222> (9)..(14)

<223> Wherein N is G, U, C or A

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 Primer Design Based on EST Sequence GenBank
 Accession Number AA281296

<400> 96
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 <212> DNA
 <213> Artificial Sequence

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 Primer Design Based on EST Sequence GenBank
 Accession Number AA281296

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<210> 98
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 <213> Artificial Sequence

<220>
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 Accession Number AA281296

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<220>
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 Accession Number AA281296

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<212> DNA
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 GenBank Accession Number AA281296

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<212> DNA

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GenBank Accession Number AA281296

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GenBank Accession Number AA281296

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 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 117
gtacatgcga cagttcgtgg ctca

24

<210> 118
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 118
catgaagcgt aggaagacgt cgaaga

26

<210> 119
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 119
cgcaaacagc ttgtttctcca tgtc

24

<210> 120
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 120
ctatgcccg acctccatca ga

22

<210> 121
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 121
ctgatggagg tccgggcata g

21

<210> 122

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 122
 cctccgaggc cgtgcagt

18

<210> 123
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 123
 cacctcaagc tttctagatc agtccaggat ggtcttgaag tca

43

<210> 124
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 124
 ggaaggcaaa ggagggcagg gcga

24

<210> 125
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 125
 cacgaattcg gatccaagct tttttttttt tttttt

37

<210> 126
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 126
gggttgcgga gggtgggc 18

<210> 127
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 127
gcagtgggtga gccgagtcct g 21

<210> 128
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 128
cgactttgga ggtgccttca 20

<210> 129
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 129
gctggtgcag cgcggggacc 20

<210> 130
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 130

gaggtgcaga gcgactactc ca 22

<210> 131
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 131
 gtctcacctc gaggtgaag 20

<210> 132
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 132
 ggctgctcct gcgtttggtg ga 22

<210> 133
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 133
 gccagagatg gagccaccc 19

<210> 134
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 134
 gggtggtccc atctctggc 19

<210> 135
 <211> 21
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 135

ccgcacgctc atcttccacg t

21

<210> 136

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 136

gcttggggat gaagcggtc

19

<210> 137

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 137

cgcttgagct gtactttgtc a

21

<210> 138

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 138

cacctcaagc tttctagatc agctagcggc ccagcccaac tcccct

46

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence

GenBank Accession Number AA281296

<400> 139
gcagcacaca tgcgtgaaac ctgt

24

<210> 140
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 140
gtgtcagaga tgacgcgcag gaa

23

<210> 141
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 141
accacacatt gcctgtcctg agt

23

<210> 142
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 142
actggatcct tgacaattaa tgcacgcggt cgtataatgt gtggagggtt gcggagggtg 60
ggc 63

<210> 143
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 143
ctgtaatacg actcactata gggttcgga gggtgggc

38

<210> 144
 <211> 73
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 144
 cacctgcaga catgcgtttc gtcttcacgg actcatcagg ccagctggcg acgcatgtgt 60
 gagccgagtc ctg 73

<210> 145
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 145
 ggatccgccg cagagcaccg tctg

24

<210> 146
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 146
 cgaagctttc agtgggccgg catctgaac

29

<210> 147
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 147
 cgaagctttc acaggcccag cccaactcc

29

<210> 148
 <211> 26
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 148

gcggatccag agccacgtcc tacgtc

26

<210> 149

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 149

gcggatccgt tcagatgccg gcccac

26

<210> 150

<211> 9

<212> PRT

<213> Homo sapiens

<400> 150

Pro Glu Met Glu Pro Pro Arg Arg Pro
1 5

<210> 151

<211> 4

<212> PRT

<213> Homo sapiens

<400> 151

Ala Ala Glu His
1

<210> 152

<211> 6

<212> PRT

<213> Homo sapiens

<400> 152

Val Gln Met Pro Ala His
1 5

<210> 153

<211> 5

<212> PRT

<213> Homo sapiens

<400> 153
Val Gly Leu Gly Leu
1 5

<210> 154
<211> 4
<212> PRT
<213> Homo sapiens

<400> 154
Arg Ala Thr Ser
1

<210> 155
<211> 622
<212> PRT
<213> Homo sapiens

<220>
<223> N-Terminal Truncated Telomerase (ver.2); encoded
by SEQ ID NO:51, with Y Intron ORF3

<400> 155
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15
His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80
Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95
Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg

165										170					175				
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu				
			180					185					190						
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro				
		195					200					205							
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala				
	210					215					220								
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser				
225					230					235					240				
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg				
				245					250					255					
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro				
			260					265					270						
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly				
		275						280					285						
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe				
	290					295					300								
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu				
305					310					315					320				
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln				
				325					330					335					
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp				
			340					345					350						
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser				
		355					360					365							
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu				
	370					375					380								
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu				
385					390					395					400				
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu				
				405					410					415					
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly				
			420					425					430						
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro				
		435					440					445							
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys				
	450					455					460								
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg				

465

470

475

480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 610 615 620

Sub D10
continued